GRADUATE AND POST-DOCTORAL FELLOWSHIPS EVOLUTIONARY MECHANISMS

Six core faculty (V. Chandler, L. Heisler, R. Lande, M. Lynch, E. Selker, and F. Stahl) in the Department of Biology, University of Oregon, are administering a five-year National Science Foundation training grant for studies on genetic mechanisms of evolution. We are seeking highly qualified, post-doctoral candidates for research associate positions and graduate student candidates for graduate research fellow positions, Some opportunity also exists for partial support of visitors on sabbatical. A sincere commitment to the understanding of both molecular genetics and evolution at the phenotypic level is an essential requirement for appointment. Applicants should submit a brief summary of interests, curriculum vitae, and names, addresses, and phone numbers of three references. The University of Oregon is an equal opportunity, affirmative action institution, committed to cultural diversity. Further information can be obtained from any of the faculty. Send applications to: Evolutionary Mechanisms Training Group, Department of Biology, University of Oregon, Eugene, OR 97403 USA.

EMINENT ECOLOGIST SEMINAR SERIES

Michigan State University's W. K. Kellogg Biological Station

Summer 1991

Speakers for the Eminent Ecologist Seminar Series:
Jim Brown, July 1–5, University of New Mexico; Seminar 1: Long-Term Experiments in Community Ecology; Seminar 2: Macroecology: The Assembly of Continental Biotas.

Astrid Kodric-Brown, July 1–5, University of New Mexico; Seminar: Mating Systems and Sexual Selection.

John Endler, July 15–19, University of California, Santa Barbara; Seminar 1: Ambient Light Effects on Color Pattern Selection; Seminar 2: Implications of the Color of Forest Light.

Sally Holbrook, July 29–August 2, University of California, Santa Barbara; Seminar: Behavioral Ecology of Marine Fishes.

Russ Schmitt, July 29–August 2, University of California, Santa Barbara; Seminar: Indirect Effects in Marine Communities.

Pam Matson, August 12–16, NASA Ames Research Center; Seminar: Atmosphere-Biosphere Interactions.

Peter Vitousek, August 12–16, Stanford University; Population-Ecosystem Interactions.

In addition to the seminar course, a variety of field ecology courses are available this summer at the Kellogg Biological Station. These courses run for five weeks, from June 19–July 23 or from July 25–August 28. They include: Field Plant Systematics, Comparative Limnology, Invertebrates, Ornithology, Topics in Conservation Biology, Scientific Illustration, Outdoor Environmental Studies, Animal Ecology, Aquatic and Wetland Plants, Plant Ecology, Ecology of Zooplankton, Plant Population Biology, Scientific Photography, and a Global Change Seminar.

Correspondence: Jan Eberhardt, Academic Coordinator
Room 3, Natural Science Building
Michigan State University
East Lansing, MI 48824
USA
(517) 355-1284

Evolution, 44(8), 1990, pp. 2164–2173

SUBJECT INDEX TO VOLUME 44

AMPHIBIANS
- sexual selection, calls, *Physalaemus pustulosus*, sensory exploitation, Túngara frog, 305
- mating system, genetic variation, offspring performance, Woodhouse's toad, *Bufo woodhousei*, 502
- kin recognition, habitat selection, spadefoot toad tadpoles, 785
- population structure, competition, kin, *Pseudacris triseriata*, chorus frog, 1529
- feeding behavior, prey transport, tetrapods, macroevolution, *Ambystoma tigrinum*, 1542
- genetic variation, paedomorphosis, *Ambystoma talpoideum*, salamander, 1588
- paedomorphosis, *Ambystoma talpoideum*, population variation, life-history pathways, salamanders, 1604
- interaction of behavioral and morphological change, novel locomotor type, flying frogs, anurans, *Rhacophorus nigropalmatus, Rhacophorus pardalis*, 1931
- dispersal, wood frog, *Rana sylvatica*, genetic population structure, gene flow, 2047
- functional complexes, additivity in performance, flying frogs, *Rhacophorus nigropalmatus, Polypedates macrotis*, 2153

BEHAVIOR
- reproductive behavior, female buntings, isolation mechanisms, hybridization, Indigo buntings, Lazuli buntings, 332
- kin recognition, habitat selection, spadefoot toad tadpoles, 785
- climbing behavior, *Peromyscus maniculatus*, geographic variation, natural selection, gene flow, 952
- food quality, heterozygosity, fitness correlates, *Peromyscus polionotus*, oldfield mice, 1318
- infanticide, cost-benefit genetic model, mothers, 1346
- feeding behavior, prey transport, amphibian, tetrapod, macroevolution, *Ambystoma tigrinum*, 1542
- genetic correlations, migratory tendency, *Gryllus firmus*, cricket, 1787
- behavior, function, intersexes, shrimp, environmental sex determination, *Gammarus duebeni*, 1875
- dynamic modeling, behavioral ecology, 1879
- interaction of behavioral/morphological change, novel locomotor type, flying frogs, anurans, *Rhacophorus nigropalmatus, Rhacophorus pardalis*, 1931
- sexual selection, song, plumage, wood warblers, Parulinae, 1967
- altered mating behavior, Carsonian population, *Drosophila sechellia*, 2057
- obligate siblicide, boobies, food limitation, parent-offspring conflict, *Sula dactylatra*, 2069

BIRDS
- Darwin-Fisher theory, sexual selection, monogamy, 180
- reproductive behavior, female buntings, isolation mechanisms, hybridization, Indigo buntings, Lazuli buntings, 332
- olfactory-bulb size, nocturnality, 339
- female choice, red jungle fowl, *Gallus gallus*, 477
- sexual selection, female choice, lek-mating bird, Lawes' Parotia, 486
- haematophagous mite, barn swallow, *Hirundo rustica*, Hamilton and Zuk hypothesis, sexual selection, 771
- natural selection, bill characters, bill morphs, *Pyrenestes ostrinus*, African finch, 832
- genetic divergence, isolated populations, chaffinches, 981
- Fisher's sex ratio theory, hatching patterns, 1009
- mitochondrial gene trees, evolutionary relationship of Mallard and Black ducks, 1109
- frequency-dependent fitness, intraspecific nest parasitism, snow geese, *Anser caerulescens caerulescens*, 1436
- genetic variation, territoriality, *Lagopus lagopus lagopus*, willow ptarmigan, 1490
- female body size, red-winged blackbirds, timing of breeding, social competition, reproductive energetics, *Agelaius phoeniceus*, 1764
- parental quality, selection, egg size, Magellanic penguin, *Spheniscus magellanicus*, 1780
- sexual monomorphism, lek-breeding, capuchinbird, *Perissocephalus tricolor, Rupicola rupicola*, 1837
- sexual selection, song, plumage, wood warbler, Parulinae, 1967
- Haldane's rule, sex biased gene flow, hybrids, flycatchers, *Ficedula albicollis, Ficedula hypoleuca*, 2012
- obligate siblicide, boobies, food limitation, parent-offspring conflict, *Sula dactylatra*, 2069

BOOKS REVIEWED
- *Evolution and its Influence: The Herbert Spencer Lectures 1986*, 227
- *A Theory of the Evolution of Development*, 465
- *Dynamics of Dinosaurs and Other Extinct Giants*, 468
- *Reproductive Success*, 469
- *Cytology and Evolution in Parthenogenesis*, 1120
- *Reconstructing the Past: Parsimony, Evolution, and Inference*, 1121
- *Speciation and its Consequences*, 1711
- *Dynamic Modeling in Behavioral Ecology*, 1879
- *Helping and Communal Breeding in Birds: Ecology and Evolution*, 2159

CHROMOSOMAL EVOLUTION
- clines, chromosomal arrangements, *Drosophila subobscura*, South America, 218
- clonal inheritance, diploid nuclear genome, hybrid, *Phoxinus eos-neogaeus*, minnows, 1052
- colonization, America, *Drosophila subobscura*, lethal genes, O_3 inversion, 1823
- retrotransposon *Mys*, sex chromosomes, copy number containment, *Peromyscus leucopus, Peromyscus maniculatus*, 2083

COEVOLUTION
- regional, local, microgeographic allele frequency variation, apple and hawthorn populations, *Rhagoletis pomonella*, 595
- tetrodotoxin resistance, garter snakes, predator-prey response, *Taricha granulosa, Thamnophis sirtalis*, 651
- habitat selection, evolutionary game, 732
- form, function, morphology, locomotor performance, *Anolis* lizards, 1189

phylogenies, insect/plant interactions, *Phyllobrotica*, Lamiales, parallel diversification, leaf beetles, Chrysomelidae, 1389
community evolution, selection response, community level, *Tribolium castaneum, Tribolium confusum*, flour beetles, 1614
community evolution, ecological basis, community selection, *Tribolium castaneum, Tribolium confusum*, flour beetles, 1625
host range evolution, colonization, *Coronilla varia, Colias philodice*, sulfur butterfly, 1637
phylogeny, host-plant association, leaf beetle, *Ophraella*, Chrysomelidae, 1885

COMPETITION (see also ECOLOGY)
population structure, competition, kin, *Pseudacris triseriata*, chorus frog, 1529
community evolution, selection response, community level, *Tribolium castaneum, Tribolium confusum*, flour beetles, 1614
community evolution, ecological basis, community selection, *Tribolium castaneum, Tribolium confusum*, flour beetles, 1625
female body size, red-winged blackbirds, timing of breeding, social competition, reproductive energetics, *Agelaius phoeniceus*, 1764
genotype-environment interaction, climate, competition, natural population, flour beetles, *Tribolium castaneum, Tribolium confusum*, 2004

CRUSTACEANS
fluctuating selection response, freshwater copepods, *Diaptomus sanguineus*, 1796
hybrid breakdown, physiological response, mechanistic approach, copepod, *Tigriopus californicus*, 1806
hybrid breakdown, developmental time, copepod, *Tigriopus californicus*, 1814

DEVELOPMENT
method for estimating gene flow, angiosperm paternity analysis, 248
correlated response, mouse mandible, selection for body composition, 669
meristem limitation, *Polygonum arenastrum, Polygonum aviculare*, genetic correlations, fecundity, growth, 799
heterochronic variation, developmental timing, cranial ossification, poeciliid fish, Cyprinodontiformes, 1558
morphological evolution, muroid rodents, craniometric covariance, ontogeny, *Zygodontomys*, 1568
paedomorphosis, *Ambystoma talpoideum*, population variation, life-history pathways, salamanders, 1604
genetic variation, developmental constraints, *Sigmodon*, cotton rats, 1738
hybrid breakdown, developmental time, copepod, *Tigriopus californicus*, 1814
ontogenetic, florets, Poa, allometry, heterochrony, Gramineae, 1978
genetic correlation structure, directional selection, *Drosophila melanogaster*, 1990

DROSOPHILA
clines, chromosomal arrangements, *Drosophila subobscura*, South America, 218
ethanol, *Drosophila*, selection, 447
genetic variation, energy storage, *Drosophila melanogaster*, 637
statistical tests, phenograms, genetic distances, 689
frequency-dependent selection, *Drosophila*, net fitness, pseudohaploid populations, 857
reproduction isolation, correlated character, sympatry, experimental evidence, *Drosophila melanogaster*, 1140
mitochondrial DNA, introgression, *Drosophila mauritiana, Drosophila simulans*, 1272
mitochondrial DNA polymorphism, cytoplasmic incompatibility, natural populations, *Drosophila simulans*, 1383
evolutionary implications, DNA divergence, *Drosophila obscura, Drosophila affinis*, 1656
colonization, America, *Drosophila subobscura*, lethal genes, O_3 inversion, 1823
genetic correlation structure, directional selection, *Drosophila melanogaster*, 1990
altered mating behavior, Carsonian population, *Drosophila sechellia*, 2057
neutrality tests, Y-linked rDNA, genetic variation, *Drosophila melanogaster*, 2106

ECOLOGY
genotypic variation, leaf damage, *Piper arieianum*, assemblage, herbivores, 104
ecological and evolutionary stability, sperm-dependent parthenogenesis, niche overlap, sexual and asexual females, 698
habitat selection, evolutionary game, 732
constant environments, complexity of form, bryozoan polymorphism, test of hypotheses, 889
gene flow paths, *Arianta arbustorum*, spatial relationship, alpine snail, 966
reproduction isolation, correlated character, sympatry, experimental evidence, *Drosophila melanogaster*, 1140
form, function, morphology, locomotor performance, *Anolis* lizards, 1189
food quality, heterozygosity, fitness correlates, *Peromyscus polionotus*, oldfield mice, 1318
habitat choice, allelic variants, *Xiphophorus variatus*, platyfish, genetic polymorphism, 1338
spatial patterns, differentiation, gene flow, *Plantago lanceolata*, 1373
population structure, competition, kin, *Pseudacris triseriata*, chorus frog, 1529
community evolution, selection response, community level, flour beetles, *Tribolium castaneum, Tribolium confusum*, 1614
community evolution, ecological basis, community selection, flour beetles, *Tribolium castaneum, Tribolium confusum*, 1625
obligate siblicide, boobies, food limitation, parent-offspring conflict, *Sula dactylatra*, 2069

ELECTROPHORETIC VARIATION (see also VARIATION–GENETIC)
biochemical genetics, *Fundulus heteroclitus*, geographical variation, gene frequencies, killifish, 16
genetic structure, *Picea abies*, Norway spruce, morphological and allozymic variation, 38
biological and historical factors, genetic diversity, *Scutellaria angustifolia*, 54
enzyme heterozygosity, growth rate, viability, *Mytilus edulis*, blue mussels, 204

allozyme heterozygosity, phenotypic traits, land snail, *Cerion*, 210
heterozygosity, growth, bivalves, *Mytilus edulis*, 213
heterozygosity, growth, bivalves, 216
geographic pattern, genetic differentiation, host-races, *Rhagoletis pomonella*, United States and Canada, 570
regional/local/microgeographic allele frequency variation, apple and hawthorn populations, *Rhagoletis pomonella*, fruit flies, 595
genetic variation, energy storage, *Drosophila melanogaster*, 637
evolutionary history, parthenogenesis, *Cnemidophorus lemniscatus*, hybrid origin, teiid lizard, 906
gametic incompatibility, *Echinometra*, Panama, sea urchins, 933
genetic differentiation, Mallophaga, Rodentia: Geomyidae, contact zone, chewing lice, pocket gophers, 942
gene flow paths, *Arianta arbustorum*, spatial relationship, alpine snail, 966
genetic divergence, isolated populations, chaffinches, *Fringilla coelebs*, *Fringilla teydea*, 981
hybridization, cultivated rice, red rice, *Oryza sativa* L., 1000
genotypic diversity, selection, *Artemia*, asexual, brine shrimp, 1035
population structure, kinship, *Polistes*, ribosomal DNA, protein electrophoresis, 1242
evolutionary genetics, Icelandic eels, *Anguilla anguilla*, *Anguilla rostrotata*, 1254
dispersal, gene flow, allelic diversity, *Thomomys bottae*, coastal ranges of California, pocket gophers, 1283
electrophoresis, interspecific hybridization, *Aesculus pavia*, *Aesculus sylvatica*, *Aesculus flava*, genetic structure, hybrid zone, 1295
genetic differentiation, host-association, *Eurosta solidaginis*, tephritid, Diptera, *Solidago altissima*, *Solidago gigantea*, 1648
hybrid breakdown, physiological response, mechanistic approach, *Tigriopus californicus*, copepod, 1806
hybrid breakdown, developmental time, copepod, *Tigriopus californicus*, 1814
phylogeny, host-plant association, leaf beetle, *Ophraella*, Chrysomelidae, 1885
population structure, host, hybridization, subspecies, *Papilio glaucus glaucus*, *Papilio glaucus canadensis*, *Liriodendron tulipifera*, *Populus deltoides*, *Betula lutea*, eastern tiger swallowtail butterfly, 1914
inbreeding effects, *Clarkia tembloriensis*, populations, outcrossing rates, Onagraceae, 2031
allozyme divergence, Bovidae, Giraffidae, 2135

FISH
biochemical genetics, *Fundulus heteroclitus* L., geographical variation, gene frequencies, killifish, 16
mitochondrial DNA, restriction-site polymorphism, *Fundulus heteroclitus*, secondary intergradation, 27
evolutionary novelty and atavism, *Semionotus* complex, relaxed selection, colonization, 71
phenotypic plasticity, sailfin mollies, *Poecilia latipinna*, field experiments, 143
phenotypic plasticity, sailfin mollies, *Poecilia latipinna*, laboratory experiment, 157
clonal inheritance, diploid nuclear genome, hybrid, *Phoxinus eos-neogaeus*, minnows, 1052
evolutionary genetics, Icelandic eels, *Anguilla anguilla*, *Anguilla rostrotata*, 1254
allopatric origin, sympatric populations, lake whitefish, *Coregonus clupeaformis*, mitochondrial DNA, 1263
habitat choice, allelic variants, *Xiphophorus variatus*, platyfish, genetic polymorphism, 1338
heterochronic variation, developmental timing, cranial ossification, poeciliid fish, Cyprinodontiformes, 1558

FITNESS (see THEORY)

GENE FLOW
Wright's shifting-balance theory, 233
method for estimating gene flow, angiosperm paternity analysis, *Raphanus sativus*, wild radish, 248
fitness consequences of multiple paternity, wild radish, *Raphanus sativus*, 260
genetic differentiation, Mallophaga, Rodentia: Geomyidae, contact zone, chewing lice, pocket gopher, 942
gene flow paths, *Arianta arbustorum*, spatial relationship, alpine snail, 966
genetic divergence, isolated populations, chaffinches, *Fringilla coelebs*, *Fringilla teydea*, 981
relative fitness, selfed and outcrossed progeny, self-compatible, protandrous, *Sabatia angularis*, environmental variation, 1129
dispersal, gene flow, allelic diversity, *Thomomys bottae*, coastal ranges of California, pocket gopher, 1283
spatial patterns, differentiation, gene flow, *Plantago lanceolata*, 1373
population structure, host, hybridization, subspecies, *Papilio glaucus glaucus*, *Papilio glaucus canadensis*, *Liriodendron tulipifera*, *Populus deltoides*, *Betula lutea*, eastern tiger swallowtail butterfly, 1914
Haldane's rule, sex biased gene flow, hybrids, flycatchers, *Ficedula albicollis*, *Ficedula hypoleuca*, 2012
inbreeding effects, *Clarkia tembloriensis*, populations, outcrossing rates, Onagraceae, 2031
dispersal, wood frog, *Rana sylvatica*, genetic population structure, gene flow, 2047

GENETIC DRIFT
dispersal, gene flow, allelic diversity, *Thomomys bottae*, coastal ranges of California, pocket gopher, 1283
mutation load, survival of small populations, Muller's ratchet, 1725
colonization, America, *Drosophila subobscura*, lethal genes, O_3 inversion, 1823

HYBRIDIZATION
P-M hybrid dysgenesis, *P*-transformed, *Drosophila simulans*, 194
reproductive behavior, female buntings, isolating mechanisms, hybridization, Indigo buntings, Lazuli buntings, 332
evolutionary history, parthenogenesis, *Cnemidophorus lemniscatus*, hybrid origin, teiid lizard, 906
evolutionary history, parthenogenesis, Amazonian lizards, *Cnemidophorus lemniscatus*, maternal origin and age, mitochondrial DNA analyses, 922

genetic differentiation, Mallophaga, Rodentia: Geomyidae, contact zone, chewing lice, pocket gopher, 942
hybridization, cultivated rice, red rice, *Oryza sativa* L., 1000
clonal inheritance, diploid nuclear genome, hybrid, *Phoxinus eos-neogaeus*, minnows, 1052
evolutionary genetics, Icelandic eels, *Anguilla anguilla, Anguilla rostrotata*, 1254
mitochondrial DNA, introgression, *Drosophila mauritiana, Drosophila simulans*, 1272
electrophoresis, interspecific hybridization, *Aesculus pavia, Aesculus sylvatica, Aesculus flava*, genetic structure, hybrid zone, 1295
variation, oviposition preference, strains, *Heliothis virescens*, 1326
molecular tests, hybrid origin, *Helianthus annus, Helianthus neglectus, Helianthus paradoxus, Helianthus petiolaris*, Asteraceae, 1498
hybridization, *Iris fulva* and *Iris hexagona*, ribosomal DNA variation, 1512
hybrids, phylogenetic systematics, character expression in hybrids, cladistic analysis, *Aphelandra*, Acanthaceae, 1685
hybrid breakdown, physiological response, mechanistic approach, copepod, *Tigriopus californicus*, 1806
hybrid breakdown, developmental time, copepod, *Tigriopus californicus*, 1814
population structure, host, hybridization, subspecies, *Papilio glaucus glaucus, Papilio glaucus canadensis, Liriodendron tulipifera, Populus deltoides, Betula lutea*, eastern tiger swallowtail butterfly, 1914
Haldane's rule, sex biased gene flow, hybrids, flycatchers, *Ficedula albicollis, Ficedula hypoleuca*, 2012
altered mating behavior, Carsonian population, *Drosophila sechellia*, 2057
hybridization, *Eucalyptus risdonii, Eucalyptus amygdalina*, 2150
hybridization, *Eucalyptus risdonii, Eucalyptus amygdalina*, 2151

INBREEDING
inbreeding depression, dominance, suppression, *Impatiens capensis*, touch-me-not, jewelweed, 269
inbreeding depression, heterozygote advantage, modifiers, outcrossing rate, 870
relative fitness, selfed and outcrossed progeny, self-compatible, protandrous, *Sabatia angularis*, environmental variation, 1129
population structure, kinship, *Polistes*, ribosomal DNA, protein electrophoresis, 1242
inbreeding depression, inbreeding coefficient effect, *Mimulus guttatus, Mimulus nasutus*, 1230
relatedness estimators, 1378
distance from parental site, offspring performance, inbreeding depression, *Impatiens capensis*, local adaptation hypothesis 2022
inbreeding effects, *Clarkia tembloriensis*, populations, outcrossing rates, Onagraceae, 2031

INSECTS (see also DROSOPHILA)
quantiiative variation, wing morphology, Heliconiinae, Ithomiinae, butterflies, 86
geographical/genetic structure, life-history variation, milkweed bugs, *Oncopeltus fasciatus*, 295
sexual dimorphism, sexual selection, intrasexual and intersexual selection, *Libellula luctuosa*, 315
geographic pattern, genetic differentiation, host races, fruit flies, *Rhagoletis pomonella*, United States and Canada, 570
regional/local/microgeographic allele frequency variation, apple and hawthorn populations, *Rhagoletis pomonella*, 595
host effects on fertility and reproductive success, *Dendroctonus ponderosae*, mountain pine beetles, 609
host-plant-induced assortative mating, *Enchenopa* treehoppers, 619
insect phenology, host-plant water relations, *Enchenopa binotata*, 629
multivariate phenotypic differentiation, bottleneck lines, housefly, *Musca domestica*, 660
origin, substitution, B chromosomes, *Eyprepocnemis plorans*, grasshoppers, 747
haematophagous mite, *Hirundo rustica*, Hamilton and Zuk hypothesis, sexual selection, barn swallow, 771
selection, reaction norms, *Eurosta-Solidago* system, 820
genetic differentiation, Mallophaga, Rodentia: Geomyidae, contact zone, chewing lice, pocket gopher, 942
sex ratio adjustment, operational sex ratio, southern green stinkbug, *Nezara viridula*, 1018
intraspecific variation, sex ratios, Trivers-Hare, ants, Hymenoptera, 1026
levels of among-population divergence, mitochondrial DNA, periodical cicadas, *Magicicada*, historical biogeography, 1066
selection, multivariate, plants, resistance to herbivores, *Ipomoea purpurea*, 1177
population structure, kinship, *Polistes*, ribosomal DNA, protein electrophoresis, 1242
variation, oviposition preference, strains, *Heliothis virescens*, 1326
phylogenies, insect/plant interactions, *Phyllobrotica*, Lamiales, parallel diversification, leaf beetles, Chrysomelidae, 1389
diploid males, primitively eusocial bee, *Lasioglossum zephyrum*, 1522
community evolution, selection response, community level, flour beetles, *Tribolium castaneum, Tribolium confusum*, 1614
community evolution, ecological basis, community selection, flour beetles, *Tribolium castaneum, Tribolium confusum*, 1625
host range evolution, colonization, *Coronilla varia, Colias philodice*, sulfur butterfly, 1637
genetics differentiation, host-association, *Eurosta solidaginis*, tephritid, Diptera, *Solidago altissima, Solidago gigantea*, 1648
pollinator adaptation, oil-secreting flowers, *Rediviva, Diascia*, solitary bees, 1701
genetic correlations, migratory tendency, *Gryllus firmus*, cricket, 1787
resources, sex roles, zaprochiline tettigoniids, 1853
phylogeny, host-plant association, leaf beetle, *Ophraella*, Chrysomelidae, 1885
population structure, host, hybridization, *Papilio glaucus glaucus, Papilio glaucus canadensis, Liriodendron tulipifera, Populus deltoides, Betula lutea*, eastern tiger swallowtail butterfly, 1914

genotype-environment interaction, climate, competition, natural population, flour beetles, *Tribolium castaneum, Tribolium confusum,* 2004

LIFE HISTORY
phenotypic plasticity, *Poecilia latipinna,* field experiments, sailfin mollies, 143
phenotypic plasticity, *Poecilia latipinna,* laboratory experiment, sailfin mollies, 157
enzyme heterozygosity, growth rate, viability, *Mytilus edulis,* blue mussels, bivalves, 204
evolution of maternal investment, egg size, offspring performance, lizards, *Sceloporus occidentalis,* 279
geographic and genetic structure, life-history variation, milkweed bugs, *Oncopeltus fasciatus,* 295
evolution of human brood size, *Homo sapiens,* 438
host effects on fertility and reproductive success, *Dendroctonus ponderosae,* mountain pine beetles, 609
flowering time variation, desert annual, *Eriogonum abertianum* TORR., Polygonaceae, 1404
paedomorphosis, *Ambystoma talpoideum,* population variation, life-history pathways, salamanders, 1604
quantitative genetics, size, shape, life-history, fruit characteristics, seed heteromorphism, *Heterosperma pinnatum,* correlation structure, 1748

MACROEVOLUTION
biogeography, North American arid regions, mitochondrial DNA phylogeny, *Onychomys,* grasshopper mice, 1
quantitative variation, wing morphology, Heliconiinae, Ithomiinae, butterflies, 86
feeding behavior, prey transport, amphibian, tetrapod, macroevolution, *Ambystoma tigrinum,* 1542

MOLECULAR EVOLUTION
biogeography, North American arid regions, mitochondrial DNA phylogeny, *Onychomys,* grasshopper mice, 1
mitochondrial DNA restriction-site polymorphism, *Fundulus heteroclitus,* secondary intergradation, fish, 27
P-M hybrid dysgenesis, *P*-transformed, *Drosophila simulans,* 194
chloroplast DNA phylogeny, *Glycine,* morphological and crossing groups, soybeans, 371
loss of chloroplast DNA inverted repeat, Papilionoideae, 390
mitochondrian DNA diversity, sea urchins, *Strongylocentrotus purpuratus, Strongylocentrotus droebachiensis,* sea urchins, 403
paramyxovirus phylogeny, tissue tropism, host specificity, 435
statistical tests, phenograms, genetic distances, 689
evolutionary history, parthenogenesis, Amazonian lizards, *Cnemidophorus lemniscatus,* maternal origin and age, mitochondrial DNA analyses, 922
genotypic diversity, selection, *Artemia,* asexual, brine shrimp, 1035
clonal inheritance, diploid nuclear genome, hybrid, *Phoxinus eos-neogaeus,* minnows, 1052
levels of among-population divergence, mitochondrial DNA, periodical cicadas, *Magicicada,* historical biogeography, 1066
restriction fragment analysis, pine phylogeny, *Pinus,* 1081
evolutionary analysis, carboxylase (*rbcL*) nucleotide sequence, grasses, Gramineae, 1097
mitochondrial gene trees, evolutionary relationship of Mallard and Black ducks, 1109
population structure, kinship, *Polistes,* ribosomal DNA, protein electrophoresis, 1242
evolutionary genetics, Icelandic eels, *Anguilla anguilla, Anguilla rostrotata,* 1254
allopatric origin, sympatric populations, lake whitefish, *Coregonus clupeaformis,* mitochondrial DNA, 1263
mitochondrial DNA, introgression, *Drosophila mauritiana, Drosophila simulans,* 1272
mitochondrial DNA polymorphism, cytoplasmic incompatibility, natural populations, *Drosophila simulans,* 1383
molecular tests, hybrid origin, *Helianthus annus, Helianthus neglectus, Helianthus paradoxus, Helianthus petiolaris,* Asteraceae, 1498
hybridization, *Iris fulva* and *Iris hexagona,* ribosomal DNA variation, 1512
evolutionary implications, DNA divergence, *Drosophila obscura, Drosophila affinis,* 1656
Haldane's rule, sex biased gene flow, hybrids, flycatchers, *Ficedula albicollis, Ficedula hypoleuca,* 2012
phylogenetic analysis, chloroplast DNA, higher taxonomic levels, Asteraceae, 2089
neutrality tests, Y-linked rDNA, genetic variation, *Drosophila melanogaster,* 2106

MOLLUSKS
enzyme heterozygosity, growth rate, viability, *Mytilus edulis,* blue mussels, bivalves, 204
allozyme heterozygosity, phenotypic traits, land snail, *Cerion,* 210
heterozygosity, growth, bivalves, *Mytilus edulis,* 213
heterozygosity, growth, bivalves, 216
coil polymorphism, snail, *Partula suturalis,* sympatric speciation, 459
gene flow paths, alpine snail, *Arianta arbustorum,* spatial relationship, 966

PALEONTOLOGY
evolutionary novelty and atavism, *Semionotus* complex, relaxed selection, colonization, 71
individual variation, Miocene *Globorotalia,* 416

PARASITISM
paramyxovirus phylogeny, tissue tropism, host specificity, 435
regional/local/microgeographic allele frequency variation, apple and hawthorn populations, *Rhagoletis pomonella,* 595
host effects on fertility and reproductive success, *Dendroctonus ponderosae,* mountain pine beetles, 609
host-plant-induced assortative mating, *Enchenopa* treehoppers, 619
haematophagous mite, *Hirundo rustica,* Hamilton and Zuk hypothesis, sexual selection, barn swallow, 771
genetic differentiation, Mallophaga, Rodentia: Geomyidae, contact zone, chewing lice, pocket gopher, 942
frequency-dependent fitness, intraspecific nest parasitism, snow geese, *Anser caerulescens caerulescens,* 1436

PHYLOGENY
biogeography, North American arid regions, mitochondrial DNA phylogeny, *Onychomys*, grasshopper mice, 1
biological and historical factors, genetic diversity, *Scutellaria angustifolia*, 54
olfactory-bulb size, nocturnality, birds, 339
gene genealogies, organismal pedigrees, random-mating, 360
chloroplast DNA phylogeny, *Glycine*, morphological and crossing groups, soybeans, 371
loss of chloroplast DNA inverted repeat, Papilionoideae, 390
mitochondrian DNA diversity, sea urchins, *Strongylocentrotus purpuratus, Strongylocentrotus droebachiensis*, sea urchins, 403
paramyxovirus phylogeny, tissue tropism, host specificity, 435
methods, correlated evolution, binary characters, gains or losses on a phylogenetic tree, 539
phylogenetic analysis, character displacement, *Anolis* lizards, 558
statistical tests, phenograms, genetic distances, 689
evolutionary history, parthenogenesis, Amazonian lizards, *Cnemidophorus lemniscatus*, material origin and age, mitochondrial DNA analyses, 922
gametic incompatibility, *Echinometra*, Panama, sea urchins, 933
levels of among-population divergence, mitochondrial DNA, periodical cicadas, *Magicicada*, historical, biogeography, 1066
restriction fragment analysis, pine phylogeny, *Pinus*, 1081
evolutionary analysis, carboxylase (*rbcL*) nucleotide sequence, grasses, Gramineae, 1097
mitochondrial gene trees, evolutionary relationship of Mallard and Black ducks, 1109
form, function, morphology, locomotor performance, *Anolis* lizards, 1189
phylogenies, insect/plant interactions, *Phyllobrotica*, Lamiales, parallel diversification, leaf beetles, Chrysomelidae, 1389
heterochronic variation, developmental timing, cranial ossification, poeciliid fish, Cyprinodontiformes, 1558
genetics differentiation, host-association, *Eurosta solidaginis*, tephritid, Diptera, *Solidago altissima, Solidago gigantea*, 1648
estimated phylogenies, tree topology, evolutionary models, Wagner trees, 1671
hybrids, phylogenetic systematics, character expression in hybrids, cladistic analysis, *Aphelandra*, Acanthaceae, 1685
phylogeny, host-plant association, leaf beetle, *Ophraella*, Chrysomelidae, 1885
phylogenetic analysis, chloroplast DNA, higher taxonomic levels, Asteraceae, 2089
allozyme divergence, Bovidae, Giraffidae, 2135

PHYSIOLOGY
sexual selection, calls, *Physalaemus pustulosus*, sensory exploitation, Túngara frog, 305
olfactory-bulb size, nocturnality, birds, 339
intraclonal variation, morphology, growth rate, copper tolerance, *Funaria hygrometrica*, moss, 441
ethanol, *Drosophila*, selection, 447
insect phenology, host-plant water relations, *Enchenopa binotata*, 629
genetic variation, energy storage, *Drosophila melanogaster*, 637
tetrodotoxin resistance, garter snakes, predator and prey response, *Taricha granulosa, Thamnophis sirtalis*, 651
differential seed production, *Mimulus guttatus*, copper tolerance, 1424
female body size, red-winged blackbirds, timing of breeding, social competition, reproductive energetics, *Agelaius phoeniceus*, 1764
genetic correlations, migratory tendency, *Gryllus firmus*, cricket, 1787
hybrid breakdown, physiological response, mechanistic approach, copepod, *Tigriopus californicus*, 1806
genotype-environment interaction, climate, competition, natural population, flour beetles, *Tribolium castaneum, Tribolium confusum*, 2004

PLANTS (see also REPRODUCTION–PLANT)
biogeography, North American arid regions, mitochondrial DNA phylogeny, *Onychomys*, grasshopper mice, 1
genetic structure, *Picea abies*, morphological and allozyme variation, Norway spruce, 38
biological and historical factors, genetic diversity, *Scutellaria angustifolia*, 54
genotypic variation, leaf damage, *Piper arieianum*, assemblage, herbivores, 104
sex-ratio variation, *Hebe strictissima*, 134
inbreeding depression, dominance, suppression, *Impatiens capensis*, touch-me-not, jewelweed, 269
chloroplast DNA phylogeny, *Glycine*, morphological and crossing groups, soybeans, 371
loss of chloroplast DNA inverted repeat, Papilionoideae, 390
intraclonal variation, morphology, growth rate, copper tolerance, *Funaria hygrometrica*, moss, 441
host-plant-induced assortative mating, *Enchenopa* treehoppers, 619
insect phenology, host-plant water relations, *Enchenopa binotata*, 629
meristem limitation, *Polygonum arenastrum*, genetic correlations, fecundity, growth, 799
selection, reaction norms, *Eurosta-Solidago* system, 820
pollen size, fertilization ability, postfertilization siring ability, *Erythronium grandiflorum*, 843
hybridization, cultivated rice, red rice, *Oryza sativa* L., 1000
restriction fragment analysis, pine phylogeny, *Pinus*, 1081
evolutionary analysis, carboxylase (*rbcL*) nucleotide sequence, grasses, Gramineae, 1097
relative fitness, selfed and outcrossed progeny, self-compatible, protandrous, *Sabatia angularis*, environmental variation, 1129
selection, multivariate, plants, resistance to herbivores, *Ipomoea purpurea*, 1177
inbreeding depression, inbreeding coefficient effect, *Mimulus guttatus, Mimulus nasutus*, 1230
electrophoresis, interspecific hybridization, *Aesculus pavia, Aesculus sylvatica, Aesculus flava*, genetic structure, hybrid zone, 1295

pollen loads, progeny vigor, *Cucurbita pepo*, Black Beauty bush zucchini, 1358
spatial patterns, differentiation, gene flow, *Plantago lanceolata*, 1373
phylogenies, insect/plant interactions, *Phyllobrotica*, Lamiales, parallel diversification, leaf beetles, Chrysomelidae, 1389
flowering time variation, desert annual, *Eriogonum abertianum* Torr., Polygonaceae, 1404
paternity analysis, *Asclepias exaltata*, multiple paternity, functional gender, pollen donation, poke milkweed, 1454
molecular tests, hybrid origin, *Helianthus annus*, *Helianthus neglectus*, *Helianthus paradoxus*, *Helianthus petiolaris*, Asteraceae, 1498
hybridization, *Iris fulva* and *Iris hexagona*, ribosomal DNA variation, 1512
host range evolution, colonization, *Coronilla varia*, *Colias philodice*, sulfur butterfly, 1637
genetics differentiation, host-association, *Eurosta solidaginis*, tephritid, Diptera, *Solidago altissima*, *Solidago gigantea*, 1648
hybrids, phylogenetic systematics, character expression in hybrids, cladistic analysis, *Aphelandra*, Acanthaceae, 1685
quantitative genetics, size, shape, life-history, fruit characteristics, seed heteromorphism, *Heterosperma pinnatum*, correlation structure, 1748
pleiotropy theory, polymorphism, disease resistance genes, plants, *Amphicarpia bracteata*, hogpeanut, *Synchytrium decipiens*, 1872
phylogeny, host-plant association, leaf beetle, *Ophraella*, Chrysomelidae, 1885
ontogenetic, florets, Poa, allometry, heterochrony, Gramineae, 1978
distance from parental site, offspring performance, inbreeding depression, *Impatiens capensis*, local adaptation hypothesis, 2022
inbreeding effects, *Clarkia temblorienses*, populations, outcrossing rates, Onagraceae, 2031
phylogenetic analysis, chloroplast DNA, higher taxonomic levels, Asteraceae, 2089

PROKARYOTES
evolution, transposable elements, establishment, bacteria, *Escherichia coli*, 347

QUANTITATIVE GENETICS
soft selection, genetic variation, quantitative trait, 168
Darwin-Fisher theory, sexual selection, monogamy, birds, 180
tetrodotoxin resistance, garter snakes, predator and prey response, *Taricha granulosa*, *Thamnophis sirtalis*, 651
multivariate phenotypic differentiation, bottleneck lines, housefly, *Musca domestica*, 660
correlated response, development, mouse mandible, selection for body composition, 669
quantitative variation, finite parthenogenetic populations, Muller's ratchet, recombination, *Drosophila*, 715
multiple equilibria, maintenance of additive genetic variance, model of pleiotropy, 1153
morphological evolution, muroid rodents, craniometric covariance, ontogeny, *Zygodontomys*, 1568
genetic variation, paedomorphosis, *Ambystoma talpoideum*, salamander, 1588
quantitative genetics, size, shape, life-history, fruit characteristics, seed heteromorphism, *Heterosperma pinnatum*, correlation structure, 1748
genetic correlation structure, directional selection, *Drosophila melanogaster*, 1990

REPRODUCTION–ANIMAL
reproductive behavior, female buntings, isolation mechanisms, hybridization, 332
heterozygosity, deer fetuses, loci, 454
mating system, genetic variation, offspring performance, Woodhouse's toad, *Bufo woodhousei*, 502
host effects on fertility and reproductive success, *Dendroctonus ponderosae*, mountain pine beetles, 609
ecological and evolutionary stability, sperm-dependent parthenogenesis, niche overlap, sexual and asexual females, 698
clonal inheritance, diploid nuclear genome, hybrid, *Phoxinus eos-neogaeus*, minnows, 1052
reproduction isolation, correlated character, sympatry, experimental evidence, *Drosophila melanogaster*, 1140

REPRODUCTION–PLANT
pollination ecotypes, *Platanthera ciliaris*, yellow-fringed orchid, 121
inbreeding depression, dominance, suppression, *Impatiens capensis*, touch-me-not, jewelweed, 269
pollen size, fertilization ability, postfertilization siring ability, *Erythronium grandiflorum*, 843
relative fitness, selfed and outcrossed progeny, self-compatible, protandrous, *Sabatia angularis*, environmental variation, 1129
pollen loads, progeny vigor, *Cucurbita pepo*, Black Beauty bush zucchini, 1358
flowering time variation, desert annual, *Eriogonum abertianum* Torr., Polygonaceae, 1404
differential seed production, *Mimulus guttatus*, copper tolerance, 1424
paternity analysis, *Asclepias exaltata*, multiple paternity, functional gender, pollen donation, poke milkweed, 1454
pollinator adaptation, oil-secreting flowers, *Rediviva*, *Diascia*, solitary bees, 1701
homospory, asexual reproduction, 1707
quantitative genetics, size, shape, life-history, fruit characteristics, seed heteromorphism, *Heterosperma pinnatum*, correlation structure, 1748

REPTILES
evolution of maternal investment, egg size, offspring performance, lizards, *Sceloporus occidentalis*, 279
phylogenetic analysis, character displacement, *Anolis* lizards, 558
tetrodotoxin resistance, garter snakes, predator and prey response, *Taricha granulosa*, *Thamnophis sirtalis*, 651
evolutionary history, parthenogenesis, *Cnemidophorus lemniscatus*, hybrid origin, teiid lizard, 906
evolutionary history, parthenogenesis, Amazonian lizards, *Cnemidophorus lemniscatus*, maternal origin and age, mitochondrial DNA analyses, 922
form, function, morphology, locomotor performance, *Anolis* lizards, 1189
selection, locomotor performance capacity, natural population, garter snakes, *Thamnophis sirtalis fitchi*, 1204

field measures, sexual selection, male lizards, *Uta palmeri*, 1956

SELECTION–EXPERIMENTAL
ethanol, *Drosophila*, selection, 447
correlated response, development, mouse mandible, selection for body composition, 669
selection, reaction norms, *Eurosta-solidago* system, 820
frequency-dependent selection, *Drosophila*, net fitness, pseudohaploid populations, 857
reproduction isolation, correlated character, sympatry, experimental evidence, *Drosophila melanogaster*, 1140
differential seed production, *Mimulus guttatus*, copper tolerance, 1424
community evolution, selection response, community level, flour beetles, *Tribolium castaneum*, *Tribolium confusum*, 1614
community evolution, ecological basis, community selection, flour beetles, *Tribolium castaneum*, *Tribolium confusum*, 1625
genetic correlations, migratory tendency, *Gryllus firmus*, cricket, 1787
genetic correlation structure, directional selection, *Drosophila melanogaster*, 1990

SELECTION–NATURAL
evolutionary novelty and atavism, *Semionotus* complex, relaxed selection, colonization, 71
natural selection, bill characters, bill morphs, *Pyrenestes ostrinus*, African finch, 832
climbing behavior, *Peromyscus maniculatus*, geographic variation, natural selection, gene flow, 952
genotypic diversity, selection, *Artemia*, asexual, brine shrimp, 1035
selection, multivariate, plants, resistance to herbivores, *Ipomoea purpurea*, 1177
frequency-dependent fitness, intraspecific nest parasitism, snow geese, *Anser caerulescens caerulescens*, 1436
female body size, red-winged blackbirds, timing of breeding, social competition, reproductive energetics, *Agelaius phoeniceus*, 1764
parental quality, selection, egg size, Magellanic penguin, *Spheniscus magellanicus*, 1780
fluctuating selection response, freshwater copepods, *Diaptomus sanguineus*, 1796
environmental selection, intraspecific divergence, mate recognition signals, cricket frog, *Acris crepitans*, 1869
causes of natural selection, 1947
natural selection, 2157

SELECTION–SEXUAL
pollination ecotypes, *Platanthera ciliaris*, yellow-fringed orchid, 121
Darwin-Fisher theory, sexual selection, monogamy, birds, 180
sexual selection, calls, *Physalaemus pustulosus*, sensory exploitation, Túngara frog, 305
sexual dimorphism, sexual selection, intrasexual and intersexual selection, *Libellula luctuosa*, 315
female choice, red jungle fowl, *Gallus gallus*, 477
sexual selection, female choice, lek-mating bird, Lawes' Parotia, 486
mating system, genetic variation, offspring performance, Woodhouse's toad, *Bufo woodhousei*, 502
ploidy, evolution, sexual selection, haploid and diploid female choice models, 757
haematophagous mite, *Hirundo rustica*, Hamilton and Zuk hypothesis, sexual selection, barn swallow, 771
genotypic diversity, selection, *Artemia*, asexual, brine shrimp, 1035
paternity analysis, *Asclepias exaltata*, multiple paternity, functional gender, pollen donation, poke milkweed, 1454
sexual monomorphism, lek-breeding, capuchinbird, *Perissocephalus tricolor*, *Rupicola rupicola*, 1837
field measures, sexual selection, male lizards, *Uta palmeri*, 1956
sexual selection, song, plumage, wood warblers, Parulinae, 1967

SEX
method for estimating gene flow, angiosperm paternity analysis, *Raphanus sativus*, wild radish, 248
fitness consequences of multiple paternity, wild radish, *Raphanus sativus*, 260
sexual dimorphism, sexual selection, intrasexual and intersexual selection, *Libellula luctuosa*, 315
host-plant-induced assortative mating, *Enchenopa* treehoppers, 619
quantitative variation, finite parthenogenetic populations, Muller's ratchet, recombination, *Drosophila*, 715
genotypic diversity, selection, *Artemia*, asexual, brine shrimp, 1035
relative fitness, selfed and outcrossed progeny, self-compatible, protandrous, *Sabatia angularis*, environmental variation, 1129
diploid males, primitively eusocial bee, *Lasioglossum zephyrum*, 1522
sexual monomorphism, lek-breeding, capuchinbird, *Perissocephalus tricolor*, *Rupicola rupicola*, 1837
resources, sex roles, zaprochiline tettigoniids, 1853
environmental selection, intraspecific divergence, mate recognition signals, cricket frog, *Acris crepitans*, 1869
behavior, function, intersexes, shrimp, environmental sex determination, *Gammarus duebeni*, 1875
altered mating behavior, Carsonian population, *Drosophila sechellia*, 2057
retrotransposon *Mys*, sex chromosomes, copy number containment, *Peromyscus leucopus*, *Peromyscus maniculatus*, 2083

SEX–RATIO
sex-ratio variation, *Hebe strictissima*, 134
ecological and evolutionary stability, sperm-dependent parthenogenesis, niche overlap, sexual and asexual females, 698
Fisher's sex ratio theory, hatching patterns in birds, 1009
sex ratio adjustment, operational sex ratio, southern green stinkbug, *Nezara viridula*, 1018
intraspecific variation, sex ratios, Trivers-Hare, ants, Hymenoptera, 1026

SPECIATION
clines, chromosomal arrangements, *Drosophila subobscura*, South America, 218
coil polymorphism, snail, *Partula suturalis*, sympatric speciation, 459
insect phenology, host-plant water relations, *Enchenopa binotata*, 629

reproduction isolation, correlated character, sympatry, experimental evidence, *Drosophila melanogaster*, 1140
allopatric origin, sympatric populations, lake whitefish, *Coregonus clupeaformis*, mitochondrial DNA, 1263
hybridization, *Iris fulva* and *Iris hexagona*, ribosomal DNA variation, 1512
environmental selection, intraspecific divergence, mate recognition signals, cricket frog, *Acris crepitans*, 1869
altered mating behavior, Carsonian population, *Drosophila sechellia*, 2057

THEORY
soft selection, genetic variation, quantitative trait, 168
Darwin-Fisher theory, sexual selection, monogamy, birds, 180
mixed-model ANOVA, quantitative genetics, 221
Wright's shifting-balance theory, 233
method for estimating gene flow, angiosperm paternity analysis, *Raphanus sativus*, wild radish, 248
evolution, transposable elements, establishment, bacteria, *Escherichia coli*, 347
gene genealogies, organismal pedigrees, random-mating populations, 360
evolution of human brood size, *Homo sapiens*, 438
coil polymorphism, snail, *Partula suturalis*, sympatric speciation, 459
optimization models, quantitative genetics, mutation, 520
methods, correlated evolution, binary characters, gains or losses on a phylogenetic tree, 539
statistical tests, phenograms, genetic distances, 689
quantitative variation, finite parthenogenetic populations, Muller's ratchet, recombination, *Drosophila*, 715
habitat selection, evolutionary game, 732
ploidy, evolution, sexual selection, haploid and diploid female choice models, 757
inbreeding depression, heterozygote advantage, modifiers, outcrossing rate, 870
multiple equilibria, maintenance of additive genetic variance, model of pleiotropy, 1153
sexual selection, diploid populations, Fisherian model, 1164
inbreeding depression, inbreeding coefficient effect, *Mimulus guttatus*, *Mimulus nasutus*, 1230
electrophoresis, interspecific hybridization, *Aesculus pavia*, *Aesculus sylvatica*, *Aesculus flava*, genetic structure, hybrid zone, 1295
infanticide, cost-benefit genetic model, mothers, 1346
relatedness estimators, 1378
estimated phylogenies, tree topology, evolutionary models, Wagner trees, 1671
population genetics, colony formation, extinction, genetic correlations within founding groups, 1717
mutation load, survival of small populations, Muller's ratchet, 1725
pleiotropy theory, polymorphism, disease resistance genes, plants, *Amphicarpia bracteata*, hogpeanut, *Synchytrium decipiens*, 1872
dynamic modeling, behavioral ecology, 1879

VARIATION–GENETIC
biochemical genetics, *Fundulus heteroclitus* L., geographical variation, gene frequencies, killifish, 16
genetic structure, *Picea abies*, morphological and allozyme variation, Norway spruce, 38
biological and historical factors, genetic diversity, *Scutellaria angustifolia*, 54
genotypic variation, leaf damage, *Piper arieianum*, assemblage, herbivores, 104
phenotypic plasticity, *Poecilia latipinna*, laboratory experiment, sailfin mollies, 157
enzyme heterozygosity, growth rate, viability, *Mytilus edulis*, blue mussels, bivalves, 204
allozyme heterozygosity, phenotypic traits, land snail, *Cerion*, 210
heterozygosity, growth, bivalves, *Mytilus edulis*, 213
heterozygosity, growth, bivalves, 216
geographical/genetic structure, life-history variation, milkweed bugs, *Oncopeltus fasciatus*, 295
heterozygosity, deer fetuses, loci, 454
geographic pattern, genetic differentiation, host races, fruit flies, *Rhagoletis pomonella*, United States and Canada, 570
regional/local/microgeographic allele frequency variation, apple and hawthorn populations, *Rhagoletis pomonella*, 595
genetic variation, energy storage, *Drosophila melanogaster*, 637
multivariate phenotypic differentiation, bottleneck lines, housefly, *Musca domestica*, 660
correlated response, development, mouse mandible, selection for body composition, 669
quantitative variation, finite parthenogenetic populations, Muller's ratchet, recombination, *Drosophila*, 715
evolutionary history, parthenogenesis, *Cnemidophorus lemniscatus*, hybrid origin, teiid lizard, 906
gametic incompatibility, *Echinometra*, Panama, sea urchins, 933
genetic differentiation, Mallophaga, Rodentia: Geomyidae, contact zone, chewing lice, pocket gopher, 942
gene flow paths, alpine snail, *Arianta arbustorum*, spatial relationship, 966
genetic divergence, isolated populations, chaffinches, 981
hybridization, cultivated rice, red rice, *Oryza sativa* L., 1000
genotypic diversity, selection, *Artemia*, asexual, brine shrimp, 1035
inbreeding depression, inbreeding coefficient effect, *Mimulus guttatus*, *Mimulus nasutus*, 1230
population structure, kinship, *Polistes*, ribosomal DNA, protein electrophoresis, 1242
evolutionary genetics, Icelandic eels, *Anguilla anguilla*, *Anguilla rostrotata*, 1254
dispersal, gene flow, allelic diversity, *Thomomys bottae*, coastal ranges of California, pocket gopher, 1283
electrophoresis, interspecific hybridization, *Aesculus pavia*, *Aesculus sylvatica*, *Aesculus flava*, genetic structure, hybrid zone, 1295
food quality, heterozygosity, fitness correlates, *Peromyscus polionotus*, oldfield mice, 1318
variation, oviposition preference, strains, *Heliothis virescens*, 1326
habitat choice, allelic variants, *Xiphophorus variatus*, platyfish, genetic polymorphism, 1338
mitochondrial DNA polymorphism, cytoplasmic in-

compatibility, natural populations, *Drosophila simulans,* 1383
inbreeding depression, genetic load, outcrossing rates, multilocus system, linkage, 1469
genetic variation, territoriality, *Lagopus lagopus lagopus,* willow ptarmigan, 1490
diploid males, primitively eusocial bee, *Lasioglossum zephyrum,* 1522
morphological evolution, muroid rodents, craniometric covariance, ontogeny, *Zygodontomys,* 1568
genetic variation, paedomorphosis, *Ambystoma talpoideum,* salamander, 1588
host range evolution, colonization, *Coronilla varia, Colias philodice,* sulfur butterfly, 1637
genetics differentiation, host-association, *Eurosta solidaginis,* tephritid, Diptera, *Solidago altissima, Solidago gigantea,* 1648
population genetics, colony formation, extinction, genetic correlations within founding groups, 1717
genetic variation, developmental constraints, cotton rats, *Sigmodon,* 1738
quantitative genetics, size, shape, life-history, fruit characteristics, seed heteromorphism, *Heterosperma pinnatum,* correlation structure, 1748
fluctuating selection response, freshwater copepods, *Diaptomus sanguineus,* 1796
hybrid breakdown, physiological response, mechanistic approach, copepod, *Tigriopus californicus,* 1806
hybrid breakdown, developmental time, copepod, *Tigriopus californicus,* 1814
colonization, America, *Drosophila subobscura,* lethal genes, O_3 inversion, 1823
pleiotropy theory, polymorphism, disease resistance genes, plants, *Amphicarpia bracteata,* hogpeanut, *Synchytrium decipiens,* 1872
phylogeny, host-plant association, leaf beetle, *Ophraella,* Chrysomelidae, 1815
population structure, host hybridization, *Papilio glaucus glaucus, Papilio glaucus canadensis, Liriodendron tulipifera, Populus deltoides, Betula lutea,* eastern tiger swallowtail butterfly, 1914
genotype-environment interaction, climate, competition, natural population, flour beetles, *Tribolium castaneum, Tribolium confusum,* 2004
inbreeding effects, *Clarkia tembloriensis,* populations, outcrossing rates, Onagraceae, 2031
dispersal, wood frog, *Rana sylvatica,* genetic population structure, gene flow, 2047
neutrality tests, Y-linked rDNA, genetic variation, *Drosophila melanogaster,* 2106
allozyme divergence, Bovidae, Giraffidae, 2135

VARIATION–PHENOTYPIC
genetic structure, *Picea abies,* morphological and allozyme variation, Norway spruce, 38
biological and historical factors, genetic diversity, *Scutellaria angustifolia,* 54
evolutionary novelty and atavism, *Semionotus* complex, related selection, colonization, 71
quantitative variation, wing morphology, Heliconiinae, Ithomiinae, butterflies, 86
sex-ratio variation, *Hebe strictissima,* 134
phenotypic plasticity, *Poecilia latipinna,* field experiments, sailfin mollies, 143
phenotypic plasticity, *Poecilia latipinna,* laboratory experiment, sailfin mollies, 157
allozyme heterozygosity, phenotypic traits, land snail, *Cerion,* 210
heterozygosity, growth, bivalves, *Mytilus edulis,* 213
heterozygosity, growth, bivalves, 216
evolution of maternal investment, egg size, offspring performance, lizards, *Sceloporus occidentalis,* 279
geographical/genetic structure, life-history variation, milkweed bugs, *Oncopeltus fasciatus,* 295
individual variation, Miocene *Globorotalia,* 416
intraclonal variation, morphology, growth rate, copper tolerance, *Funaria hygrometrica,* moss, 441
phylogenetic analysis, character displacement, *Anolis* lizards, 558
multivariate phenotypic differentiation, bottleneck lines, housefly, *Musca domestica,* 660
pollen size, fertilization ability, postfertilization siring ability, *Erythronium grandiflorum,* 843
constant environments, complexity of form, bryozoan polymorphism, test of hypotheses, 889
climbing behavior, *Peromyscus maniculatus,* geographic variation, natural selection, gene flow, 952
selection, multivariate, plants, resistance to herbivores, *Ipomoea purpurea,* 1177
form, function, morphology, locomotor performance, *Anolis* lizards, 1189
selection, locomotor performance capacity, natural population, garter snakes, *Thamnophis sirtalis fitchi,* 1204
variation, oviposition preference, strains, *Heliothis virescens,* 1326
pollen loads, progeny vigor, *Cucurbita pepo,* Black Beauty bush zucchini, 1358
frequency-dependent fitness, intraspecific nest parasitism, snow geese, *Anser caerulescens caerulescens,* 1436
morphological evolution, muroid rodents, craniometric covariance, ontogeny, *Zygodontomys,* 1568
genetic variation, paedomorphosis, *Ambystoma talpoideum,* salamander, 1588
host range evolution, colonization, *Coronilla varia, Colias philodice,* sulfur butterfly, 1637
pollinator adaptation, oil-secreting flowers, *Rediviva, Diascia,* solitary bees, 1701
quantitative genetics, size, shape, life-history, fruit characteristics, seed heteromorphism, *Heterosperma pinnatum,* correlation structure, 1748
field measures, sexual selection, male lizards, *Uta palmeri,* 1956
distance from parental site, offspring performance, inbreeding depression, *Impatiens capensis,* local adaptation hypothesis, 2022